

FIG. 1

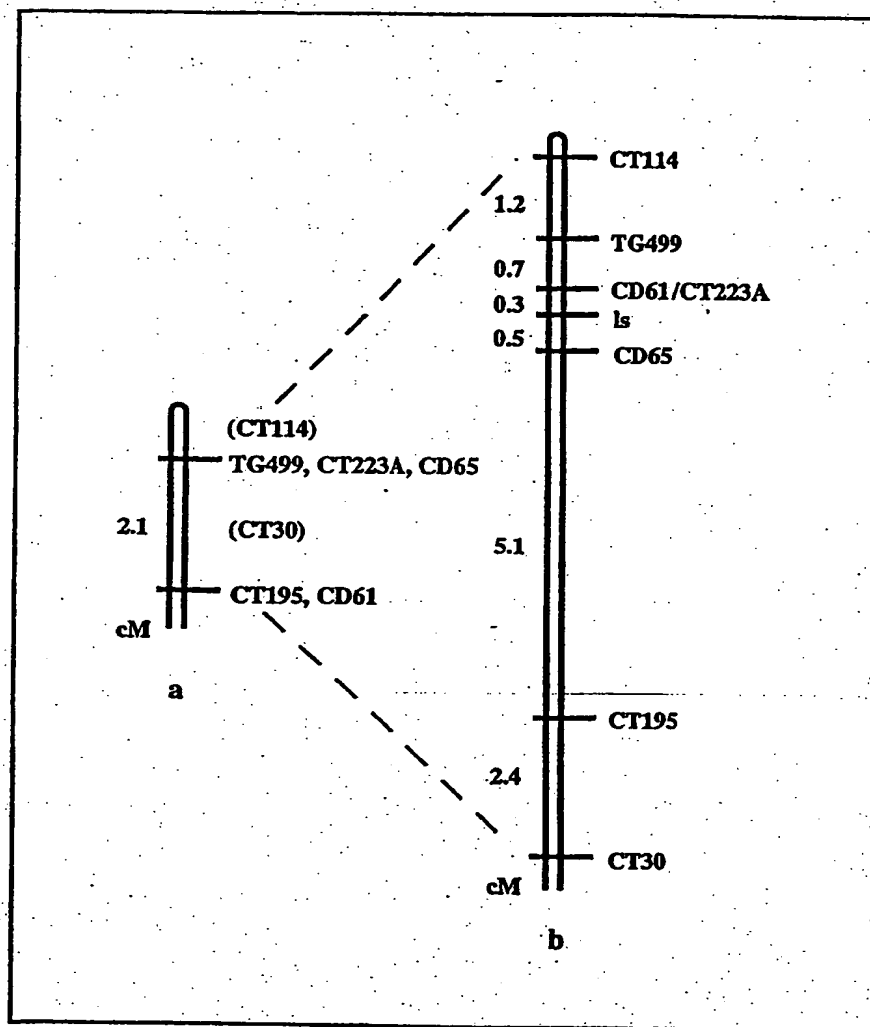


FIG. 2

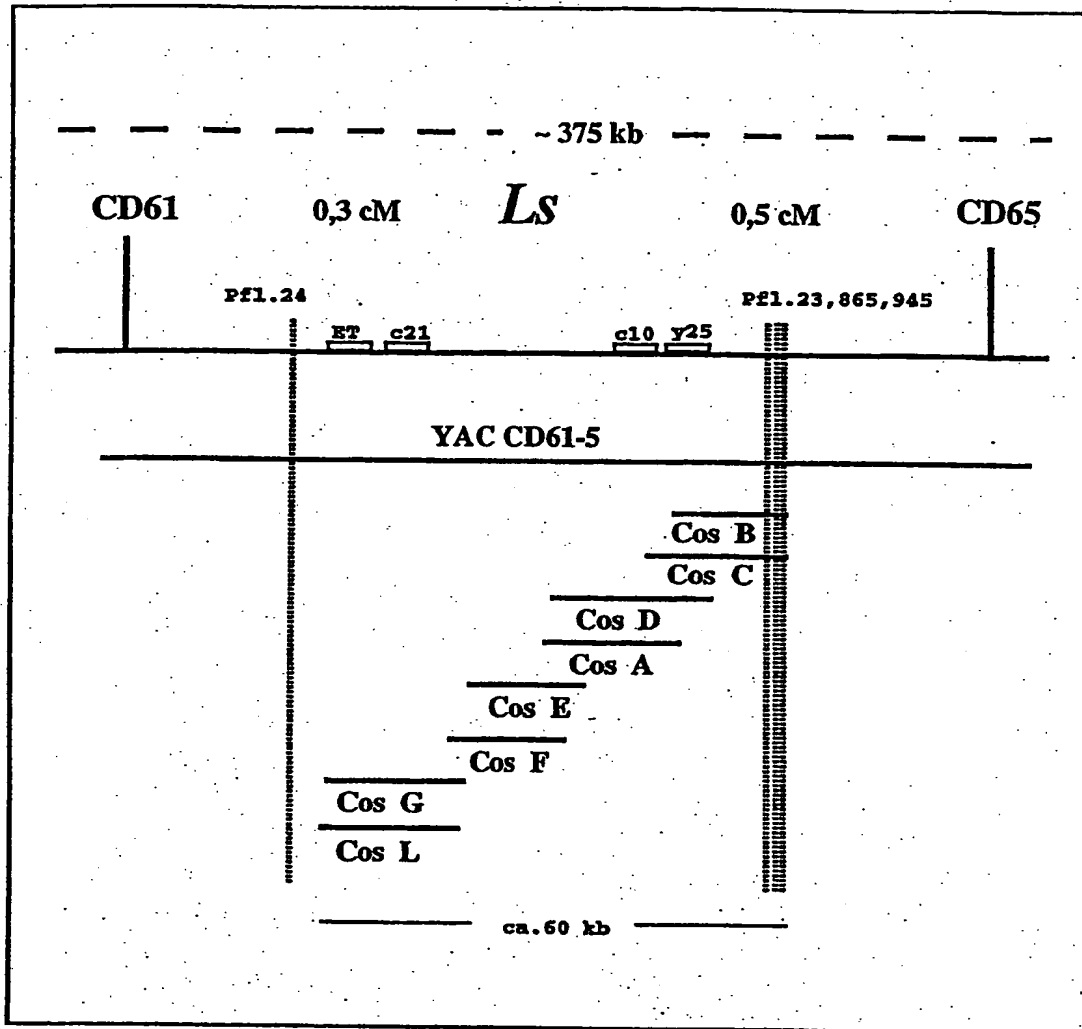


FIG. 3

A. majus
S. tuberosum
L. esculentum

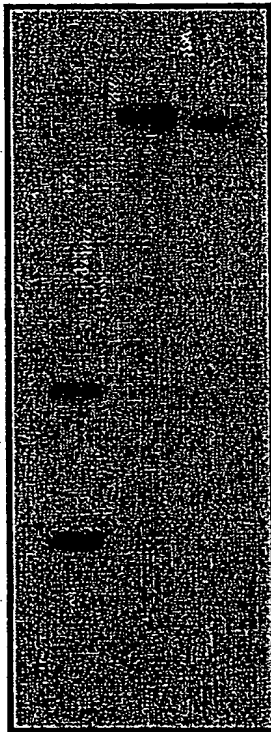


FIG. 4



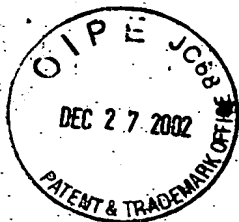
1 CCTCTGTCTCTCCCCCAGGTCCCTTTTTCCTTTCTCTCTCTCTCTTTTATTTCTCTTT 60
61 TCATAAGCATATTCTTTCTCTCTCTAGGGTTTTTCACTTTTCACCTGAAATAGTGTGTAA 120
121 ATTGAATGATATGTTAGGATCCTTTTGGTTCCTTCATCATCTCAATCTCACCCCTCATCATGA 180
M L G S F G S S S S Q S H P H H D
181 TGAAGAATCTTCTGATCATCATCAACAGCGTAGATTACCGCTACTGCTACAACTATCAC 240
E E S S D H H Q Q R R F T A T A T T I T
241 CACCACCACCATCACTACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGC 300
T T T I T T S P A I Q I R Q L L I S C A
301 GGAGTTGATTTCCGAGTCCGATTTTCTCGGCCGCGAAAAGACTCCTTACTATATTATCAAC 360
E L I S Q S D F S A A K R L L T I L S T
361 TAACTCATCTCCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAATTTACTCGGCACT 420
N S S P F G D S T E R L V H Q F T R A L
421 TTCCCTTCGTCTCAACCGCTATATATCGTCAACCACCAATCATTTCATGACACCTGTGA 480
S L R L N R Y I S S T T N H F M T P V E
481 AACAACTCCAACGTATTCTTCTCTTCGTTCATCATTAGCTCTAATTCAATCATCATATCT 540
T T P T D S S S S S S L A L I Q S S Y L
541 ATCTCTAAACCAAGTTACCCCTTTTCATAAGGTTTACTCAATTAACCGCTAATCAAGCGAT 600
S L N Q V T P F I R F T Q L T A N Q A I
601 TTTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTGACATTAAATCA 660
L E A I N G N H Q A I H I V D F D I N H
661 CGGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCCTGCTCCCACTCT 720
G V Q W P P L M Q A L A D R Y P A P T L
721 TCGAATCACCGGTACTGGAAATGACCTTGATACCCCTTCGTAGAACAGGTGATCGTTTAGC 780
R I T G T G N D L D T L R R T G D R L A
781 TAAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATAGCCAATAA 840
K F A H S L G L R F Q F H P L Y I A N N
841 TAACCACGATCAGATGAAGATCCTTCTATTATTTCTCCATTGTACTACTCCCTGATGA 900
N H D H D E D P S I I S S I V L L P D E
901 AACCTAGCTATCAACTGTGTTTTCTACCTCCACCGCTTTTAAAGACCGCGAAAAGTT 960
T L A I N C V F Y L H R L L K D R E K L
961 AAGGATTTTTTTGTCATAGGGTTAAGTCAATGAACCTAAAATTGTTACAATCGCGGAGAA 1020
R I F L H R V K S M N P K I V T I A E K
1021 GGAAGCAAATCATAACCATCCTCTTTTTTTTACAAAGATTCATCGAGGCGTTGGATTATTA 1080

FIG.5A



E A N H N H P L F L Q R F I E A L D Y Y
1081 TACAGCTGTGTTTGATTCACTGGAAGCTACATTGCCACCGGGTAGTCGAGAGAGGATGAC 1140
T A V F D S L E A T L P P G S R E R M T
1141 AGTTGAACAAGTGTGGTTTGGGAGAGAGATTGTTGATATCGTTGCGATGGAAGGAGATAA 1200
V E Q V W F G R E I V D I V A M E G D K
1201 AAGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATT 1260
R K E R H E R F R S W E V M L R S C G F
1261 TAGTAATGTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTTCA 1320
S N V A L S P F A L S Q A K L L L R L H
1321 TTATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCCTTCTTCTTAGGTTGGCA 1380
Y P S E G Y Q L G V S S N S F F L G W Q
1381 AAATCAACCCCTTTTCTCCATCTCGTCTTGGCGTTGAGAAAACTATCAAATAGCCCACT 1440
N Q P L F S I S S W R
1441 TCAGAGGGTAATTAAGACTACTGATAGTTTAGGAGGGATCTGAAGAAAACGGGTGGAGTG 1500
1501 AAAACCTAAATAACCAGATTTTCTAATGAAGTTGTAGTAGTAGAAATTTGCATGGTGAA 1560
1561 GAACAATATTGAAGAGGTATTGAAATTTCAATGTTTTTTTGTCTTACTTATTGATATGAA 1620
1621 TGTTTTAAAATTTTAAACATAGAGGACTAGGTTGATGATATATAGTATTTAAGTTAACTA 1680
1681 GTCTTTGTATAACGCAAGATCTTGATCAACTTATTTTTATTTTAAATTA 1729

FIG. 5B



1 ATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCTCATCATGATGAAGAATCT 60
1 M L G S F G S S S S Q S H P H H D E E S 20
61 TCTGATCATCATCAACGGCGTAGATTCACCGCTACTACTACAACATCACCACCACCACC 120
21 S D H H Q R R R F T A T T T T I T T T T 40
121 ACAACGACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGCGGAGTTGATT 180
41 T T T S P A I Q I R Q L L I S C A E L I 60
181 TCGCGTCCGATTCTCGGCCGCGAAAAGACTCCTTACCATATTATCAACTAATCTTCT 240
61 S R S D F S A A K R L L T I L S T N S S 80
241 CCTTTGGTGATTCAACTGAACGGTTAGTCCATCAGTTTACTCGCGCACTTTCCCTTCGT 300
81 P F G D S T E R L V H Q F T R A L S L R 100
301 CTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTTGAAACAACCTCCA 360
101 L N R Y I S S T T N H F M T P V E T T P 120
361 ACTGATTCTTCATCTTCGTTGCCATCGTCATCATTAGCTCTAATTCATCATCATATCAT 420
121 T D S S S S L P S S S L A L I Q S S Y H 140
421 TCTCTAAATCAAGTTACCCCTTTTATAAGGTTTACTCAATTAACCGCTAATCAAGCGATT 480
141 S L N Q V T P F I R F T Q L T A N Q A I 160
481 TTAGAAGCGATTAAACGGTAATCATCAAGCAATCCACATCGTTGATTTCGACATTAAATCAC 540
161 L E A I N G N H Q A I H I V D F D I N H 180
541 GGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCTACTCTT 600
181 G V Q W P P L M Q A L A D R Y P A P T L 200
601 CGAATCACCGGTACTGGAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGCT 660
201 R I T G T G N D L D T L R R T G D R L A 220
661 AAATTGCTCACTCATTAGGGTTGAGATTTCAATTCATCCTCTTTATATCGCCAATAAT 720
221 K F A H S L G L R F Q F H P L Y I A N N 240
721 AACCGCGATCACGGTGAAGATCCTTCTATTATTTCTCCATTGTACTTCTCCCTGATGAA 780
241 N R D H G E D P S I I S S I V L L P D E 260
781 ACCCTAGCTATCAACTGTGTTTCTATCTCCACCGCCTTTTAAAAGACCGCGAAAAATTA 840
261 T L A I N C V F Y L H R L L K D R E K L 280

FIG. 6A



841 AGGATTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAAG 900
281 R I F L H R V K S M N P K I V T I A E K 300
901 GAAGCAAATCATAACCATCCTCTTTTTTACAAAGATTATCGAGGCGTTGGATTATTAT 960
301 E A N H N H P L F L Q R F I E A L D Y Y 320
961 ACAGCTGTGTTTGATTCAATTGGAAGCTACATTGCCACCGGTAGTCGTGAGAGGATGACA 1020
321 T A V F D S L E A T L P P G S R E R M T 340
1021 GTTGAACAAGTGTGGTTTGGGAGAGAAATTGTTGATATCGTGGCGATGGAAGGAGATAAA 1080
341 V E Q V W F G R E I V D I V A M E G D K 360
1081 AGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATTT 1140
361 R K E R H E R F R S W E V M L R S C G F 380
1141 AGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTACAT 1200
381 S N V A L S P F A L S Q A K L L L R L H 400
1201 TATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCAA 1260
401 Y P S E G Y Q L G V S S N S F F L G W Q 420
1261 AATCAACCTCTTTTCTCCATCTCGTCTTGGCGTTGA 1296
421 N Q P L F S I S S W R * 432

FIG. 6B



1 GAGAGGTCATCAAACCCTAGCAGTCCACCTCCATCTCTCCGCATAACCGGATGCGGTCTGA 60
E R S S N P S S P P P S L R I T G C G R
61 GATGTAACCGGATTAAACCGAACTGGAGACCGGTTAACCCGGTTCGCTGACTCTTTAGGT 120
D V T G L N R T G D R L T R F A D S L G
121 CTCCAATTCCAGTTTCACACGCTAGTGATCGTAGAAGAAGATCTCGCCGGACTTTTGCTA 180
L Q F Q F H T L V I V E E D L A G L L L
181 CAGATCCGATTGTTAGCTCTCTCAGCCGTACAAGGAGAGACCATTGCCGTCAATTGTGTT 240
Q I R L L A L S A V Q G E T I A V N C V
241 CACTTCTCCACAAAATATTTAACGACGATGGAGATATGATCGGTCACTTCTTGTCAGCG 300
H F L H K I F N D D G D M I G H F L S A
301 ATCAAGAGCTTAAACTCTAGAATCGTTACAATGGCAGAGAGAGAAGCTAATCATGGAGAT 360
I K S L N S R I V T M A E R E A N H G D
361 CACTCGTTCTTGAATAGATTCTCTGAGGCAGTGGATCATTACATGGCGATCTTTGATTCTG 420
H S F L N R F S E A V D H Y M A I F D S
421 TTGGAAGCGACGTTGCCGCCAAATAGCCGAGAGAGACTAACCCCTAGAGCAACGGTGGTTC 480
L E A T L P P N S R E R L T L E Q R W F
481 GGTAAGGAGATTTTGGATGTTGTGGCGCGGAAGAGACGGAGAGAAAGCAAAGACATCGG 540
G K E I L D V V A A E E T E R K Q R H R
541 AGGTTTGAGATTTGGGAAGAGATGATGAAGAGGTTTGGTTTCGTTAACGTTCTTATTGGA 600
R F E I W E E M M K R F G F V N V P I G
601 AGCTTTGCTTTGTCTCAAGCTAAGCTTCTTCTTAGACTTCATTATCCTTCAGAAGGTTAT 660
S F A L S Q A K L L L R L H Y P S E G Y
661 AATCTTCAGTTCCTTAACAATTCTTTG 687
N L Q F L N N S L

FIG. 7

[illegible]

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LSat 1 505DFSAAKRLLTILSTNSSPFQDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP
LSLe 61 505DFSAAKRLLTILSTNSSPFQDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP
LSSt 61 505DFSAAKRLLTILSTNSSPFQDSTERLVHQFTRALSRLNRYISSSTTNHFMTPVETTP

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LSat	1	SSSLALIQSSY	SLNQVTPPIRFTQLTANQAI	LEANGNHQAII	IVDFDINH
LSle	121	SSSLALIQSSY	SLNQVTPPIRFTQLTANQAI	LEANGNHQAII	IVDFDINH
LSSt	121	SSSLALIQSSY	SLNQVTPPIRFTQLTANQAI	LEANGNHQAII	IVDFDINH

1	-----ERSSNPSSPPPPRLRITGCGGGTGLNRTGDRLLTFA	DSLGLQFQPHLTVVEE
Lsat		
178	GVQWPPLMQALADRYPPAPTLLRITGTGNDLDTLRRTGDRLLAKFAHSLGLRFFQFHPLYIANN	
Lsle		
181	EVQWPPLMQALADRYPPAPTLLRITGTGNDLDTLRRTGDRLLAKFAHSLGLRFFQFHPLYIANN	
Lsst		

Lsat	54	DLAGLLQIRL	ABVQGET	AINCVHLLH	FND	DGPEHGHFLSAKSEN	SLVTIAEE
Lsle	238	N	DHDEDP	SISSIVLLPDET	LA	INC	VFYLHRLLK
Lsst	241	N	DHDEDP	SISSIVLLPDET	LA	INC	VFYLHRLLK

LSa	114	KEANH3DHSFLRFEADYKAFDSLEATLPPNSRERATTEQWFGREI	IVAMEGDD
LSa	297	KEANHNNHPLFLQRFIEALDYTAVFDSLEATLPPGSRERMTVEQWFGREI	IVAMEGDD
LSa	300	KEANHNNHPLFLQRFIEALDYTAVFDSLEATLPPGSRERMTVEQWFGREI	IVAMEGDD

174 L8At ERKRRHRFRFEIYE34GSPFALSOAKLLRLRLHYHPSEGYQLGVSSNSFFFLGWW

357 L8L KRKERHERFRSRWEVMLRSCGFSNVALSPFALSOAKLLRLRLHYHPSEGYQLGVSSNSFFFLGWW

360 L8St KRKERHERFRSRWEVMLRSCGFSNVALSPFALSOAKLLRLRLHYHPSEGYQLGVSSNSFFFLGWW

LsAt	230	QNQPLFSISWR
LsLe	417	QNQPLFSISWR
LsSt	420	QNQPLFSISWR